

FIGURE 1

20 40 30 10 **ATGCTAGGGACCTGCCTTAGACTCCTGGTGGGCGTGCTCTGCACTGTCTGCAGCTTGGGC** M L G T C'L R L L V G V L C T V C S L G . 80 110 100 90 **ACTGCTAGAGCCTATCCAGACACTTCCCCATTGCTTGGCTCCAACTGGGGAAGCCTGACC** T A R A Y P D T S P L L G S N W G S L T 130 (140 150 170 160 CACCTGTACACGGCTACAGCCAGGACCAGCTATCACCTACAGATCCATAGGGATGGTCAT HLYTÄÄÄRTSYHLQIHRDGH 230 190 200 220 210 GTAGATGGCACCCCCATCAGACCATCTACAGTGCCCTGATGATTACATCAGAGGACGCC V D G T P H Q T I Y S A L M I T S E D A 250 760 270 290 280 GGCTCTGTGGTGATAACAGGAGCCATGACTCGAAGGTTCCTTTGTATGGATCTCCACGGC G S V V IT THE ACM T R R F L C M D L H G . 310 . - 320 330 340 AACATTTTTGGATCGCTTCACTTCAGCCCAGAGAATTGCAAGTTCCGCCAGTGGACGCTG NIFGS LANFSPENCKFRQWTL 370 380 390 400 410 GAGAÁTGGCTÁTGÁCGTÁCTTGTCGCAGAAGCATCACTACCTGGTGAGCCTGGGCCGC ENGGY, DVY, LSQKHHYLVSLGR 430 440 450 460 470 GCCAAGCGCATTTTCCAGCCGGGCACCAACCCGCCGCCCTTCTCCCAGTTCCTGGCTCGC A K, R I F QUP G T N P P P F S Q F L A R 490 ... 500 530 520 510 AGGAÁCGAGGTCCCGCTGCTGCACTTCTACACTGTTCGCCCACGGGGGCCACACGCGCAGC RNEVPLLHFYTVRPRRHTRS 580 590 570 560 GCCGAGGACCCACCCGAGCGCGACCCACTGAACGTGCTCAAGCCGCGGCCCCGCGCCACG A E D P P E R D P L N V L K P R P R A T 618 7 620 630 640 650 CCTGTGCCTGTATCCTGCTCTCGCGAGCTGCCGAGCGCAGAGGAAGGTGGCCCCGCAGCC PAIPESSRELPSAEEGGPAA 690 700 710 67.0 5 680 AGCGATCCTCTGGGGGTGCTGCGCAGAGGCCGTGGAGATGCTCGCGGGGGGCGCGGGAGGC S D P L G V L R R G R G D A R G G A G G

FIGURE 2

730 740 750 760

GCGGATAGGTGTCGCCCCTTTCCCAGGTTCGTCTAG

A D R C R P F P R F V *

Human FGF-23				
10 atgttggggg H L G A	ccoacctcaa	actctagatct	40 gtgccttgtgca A L C S	50 60 gcgtctgcagcatgagc V C S H S
70 gtcctcagag V L R A	cctateccaat	90 tgcctccccac A S P L	100 tgctcggctcca; L G S S	110 120 gctggggtggcctgatc W G G L I
. 130 cacctataca	140 caaccacaaca	150 taggaacageto	160 accacctgcagat	170 180 cccacaagaatggccat H K N G H
, 190 atagataga	Z00	210 Jaccotctaca	ZZ0 Itaccctgataat	230 240 cagatcagaggatgct R S E D A
250 aactttatäa	260 taattacaaat	270 ataataagcag	280 pagatacctctg	Z90 300 cotggatttcagaggc M D F R G
310 aacattttta	320 gatcacactat	330 ttcgacccgga	340	350 360 ccaacaccagacgctg
: 370	380	390	400 otatcacttcct	410 420 ggtcagtctgggccgg V S L G R
÷ 430·	440	450 aacatagaccc	460 accccqtactc	470 480 ccagttcctgtcccgg Q F L S R
490 aggaatgagat	500 ecccctaatt	510 cacttcaacac	520	530 540 gcggcacacccggagc
R N E I	560 ictcaáaacaa	.· 570 gaccccctgoo	580 cgtgctgaagcc	590 600 ccgggcccggatgacc RARMT
610. CCggccccggò	520 ctcctgttca	630 Caggagetece	640 gagcgccgagga	
670	aaoaataatco	 : 690 aaaacaatca	700 agtgoacacgca	710 720 cgctggggggaacgggc A G G T G
; 730		750	760 ctag	

Mouse FGF-23	MLGTCLRLLVGVLCTVCSLGTARAYPDTSPLLGSNWGSLTHLYTATARTSYHLQIHRDGH	60
Human FGF-23	MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH	66
	VDGTPHQTIYSALMITSEDAGSVVITGAMTRRFLCMDLHGNIFGSLHFSPENCKFRQWTL	120
	VDGAPHQTIYSALHIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL	128
	ENGYDVYLSQKHHYLVSLGRAKRIFQPGTNPPPFSQFLARRNEVPLLHFYTVRPRRHTRS	186
	ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS	186
	AEDPPERDPLNVLKPRPRATPVPVSCSRELPSAEEGGPAASDPLGVLRRGRGDARGGAGG	240
	A EDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG	240
	ADRCRPFPRFV 251 *****.	
	PEGCRPFAKFI 251	

Human FGF-23	MLGAREREWVCALCSVCSMSVLRAYPNASPLEGSSWGGLIHLYTATARNSYHL	53
Human FGF-19	MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFL	60
	QIHKNGHYDGAPHQTIYSALMIRSEDAGFYYITGVMSRRYLCMDFRGNIFGSHYFDPENC	113
	DED AD CARDO LOCACIONELLO CENTRALIDADA EN CARDO COMO CARDO C	120
	RFQHQTLENGYDVYHSPQYHFLVSLGRAK-RAFLPGHNPPPYSQFLSRRHEIPLIHFNTP *	172
	AFEEEIRPDGYNYYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLR	180
	IPRRHTRSAEDDSERDPLNVLKPRARHTPAPASCSQELPSAEDNSPHASDPLGVVRGGRV	232
	GHLESDMFSSPLETDSMDPFGLVTGLEAVRSPSFEK	216
	NTHAGGTGPEGCRPFAKFI	251

Human FGF-2	3 HEGARLREWVCALCS-VCSMSVERAYPNASPLEG-SSWGGLIHLYTATARNS-YH	52
Human FGF-2		60
	LQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPEN	112
	LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA	120
	CRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTP	172
	CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP-HRDPAPRGPARFLPLPGLPPALPEP	177
	IPRRHTRSAEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRV	232
	-PGILAPQPPDVGSSDPLSMVGPSQGRSPSYAS	209
	NTHAGGTGPEGCRPFAKFI	251

 $\begin{tabular}{ll} Figure 7 \\ \hline \end{tabular}$ Codon usage for yeast (highly expressed) genes

AmAcid	Codon	Number	/1000	Fraction .
Gly	GGG	33 00	0 86	0.01
Gly	GGA	70 00	1 82	0.02
Gly	GGT	2672 00	69 62	0.91
Gly	GGC	171 00	4 46	0.06
Glu	GAG	277 00	7 22	0 10
Glu	GAA	2442 00	63 63	0 90
Asp	GAT	1100 00	28.66	0 48
Asp	GAC	1211 00	31 55	0 52
Val Val Val	GTG GTA GTT GTC	117 00 75 00 1548 00 1026 00	3 05 1.95 40.33 26.73	0 04 0 03 0 56 0 37
Ala	GCG	36 00	0 94	0 01
Ala	GCA	203 00	5 29	0.06
Ala	GCT	2221 00	57 87	0 65
Ala	GCC	969.00	25 25	0 28
Arg	AGG	20 00	0.52	0 01
Arg	AGA	1336.00	34 81	0 83
Ser	AGT	116 00	3.02	0 05
Ser	AGC	94 00	2 45	0 04
Lys	AAG	2365 00	61 62	0 78
Lys	AAA	651 00	16 96	0 22
Asn	AAT	347 00	9 04	0 22
Asn	AAC	1259.00	32.80	0.78
Met	ATG	766 00	19.96	1.00
Ile	ATA	43.00	1.12	0.02
Ile	ATT	1223.00	31.87	0.52
Ile	ATC	1070.00	27.88	0.46
Thr	ACG	28 00	0 73	0.01
Thr	ACA	126 00	3 28	0.06

Figure 7 (continued)

Thr	ACT	1129 00	29.42	0 50
Thr	ACC	962.00	25.07	0.43
Trp	TGG	325 00	8 47	1 00
End	TGA	10 00	0.26	0.09
Cys	TGT	254.00	6.62	0 89
Cys	TGC	33 00	0.86	0 11
End	TAG	11 00	0.29	0 10
End	TAA	85 00	2 21	0.80
Tyr	TAT	219 00	5 71	0 19
Tyr	TAC	913 00	23 79	0 81
Leu	TTG	2202.00	57 38	0 69
Leu	TTA	576 00	15 01	0 18
Phe	TTT	432 00	11 26	0 27
Phe	TTC	1145 00	29 83	0 73
Ser Ser Ser	TCG TCA TCT TCC	26 00 149 00 1279 00 818 00	0 68 3 88 33.33 21 31	0 01 0 06 0 52 0 33
Arg	CGG	0 00	0 00	0 00
Arg	CGA	1 00	0 03	0 00
Arg	CGT	249.00	6 49	0 15
Arg	CGC	5 00	0 13	0 00
Gln	CAG	62 00	1 62	0 05
Gln	CAA	1225 00	31 92	0 95
His	CAT	236 00	6 15	0 35
His	CAC	433 00	11 28	0 65
Leu	CTG	52 00	1 35	0 02
Leu	CTA	236 00	6 15	0.07
Leu	CTT	90 00	2.35	0.03
Leu	CTC	14.00	0.36	0.00
Pro	CCG	10 00	0.26	0 01
Pro	CCA	1271.00	33.12	0 80
Pro	CCT	279.00	7.27	0.18
Pro	CCC	33 00	0.86	0.02

 $Figure \ 8$ Codon usage for Drosophila (highly expressed) genes

AmAc1d	Codon	Number	/1000	Fraction	
Gly	GGG	6 00	0.28	0 00	
Gly	GGA	380 00	18.04	0 22	
Gly	GGT	575 00	27.29	0 34	
Gly	GGC	746 00	35 41	0 44	
				0.01	
Glu	GAG	1217 00	57.77	0 91	
Glu	GAA	115 00	5 46	0 09	
Asp	GAT	503 00	23.88	0 43	
Asp	GAC	654 00	31 04	0 57	
		710 00	21 12	0 45	
Val	GTG	719 00	34 13	0 43	
Val	GTA	29 00	1 38		
Val	GTT	226 00	10 73		
Val	GTC	608 00	28 86	0 38	
Ala	GCG	94 00	4 46	0 05	
Ala	GCA	80 00	3 80	0 04	
Ala	GCT	446 00	21 17	0 24	
	GCC	1277.00	60 61	0 67	
Ala	acc	12/7.00	00 01	0 0	
Arg	AGG	48 00	2 28	0 06	
Arg	AGA	12 00	0 57	0 01	
Ser	AGT	16 00	0 76	0 01	
Ser	AGC	267 00	12 67	0 23	
Lys	AAG	1360 00	64 55	0 93	
Lys	AAA	108 00	5 13	0 07	
Asn	AAT	127 00	6 03	0 13	
Asn	AAC	878 00	41.67	0.87	
			10 07	1 00	
Met	ATG	387 00	18.37	1.00	
Пe	ATA	4.00	0 19	0.00	
He	ATT	390 00	18.51	0 29	
He	ATC	969.00	45.99	0.71	
77.1	100	114.00	C ∆1	0.08	
Thr	ACG	114 00	5.41	0.08	
Thr	ACA	34 00	1.61	U.UZ	

Figure 8 (continued)

Thr	ACT	164 00	7 78	0 11
Thr	ACC	1127.00	53 49	0 78
Trp	TGG	243 00	11 53	1 00
End	TGA	1 00	0 05	0.01
Cys	TGT	20 00	0.95	0 08
Cys	TGC	220 00	10 44	0 92
End	TAG	12 00	0 57	0.17
End	TAA	58 00	2 75	0 82
Tyr	TAT	113 00	5.36	0 16
Tyr	TAC	574 00	27.25	0 84
Leu	TTG	210.00	9 97	0.12
Leu	TTA	9 00	0.43	0 01
Phe	TTT	62 00	2 94	0 09
Phe	TTC	635.00	30 14	0 91
Ser	TCG	195 00	9 26	0.17
Ser	TCA	29 00	1 38	0 02
Ser	TCT	103 00	4 89	0 09
Ser	TCC	558 00	26.49	0 48
Arg	CGG	7 00	0 33	0 01
Arg	CGA	25 00	1 19	0 03
Arg	CGT	281 00	13.34	0 34
Arg	CGC	465 00	22 07	0.55
Gln	CAG	703 00	33 37	0 91
Gln	CAA	66.00	3 13	0 09
His	CAT	88 00	4 18	0 22
His	CAC	312 00	14 81	0 78
Leu	CTG	1182 00	56 10	0 69
Leu	CTA	21 00	1 00	0 01
Leu	CTT	55 00	2.61	0.03
Leu	CTC	224.00	10.63	0 13
Pro	CCG	84 00	3.99	0.09
Pro	CCA	135.00	6.41	0.15
Pro	CCT	72 00	3.42	0.08
Pro	CCC	626.00	29.71	0.68

Figure 9 Codon usage for enteric bacterial (highly expressed) genes 7/19/83

	5			
AmAcıd	Codon	Number	/1000	Fraction
Gly Gly Gly	GGG GGA GGU GGC	13.00 3 00 365 00 238 00	1.89 0.44 52.99 34.55	0 02 0 00 0 59 0.38
Glu	GAG	108 00	15 68	0 22
Glu	GAA	394.00	57 20	0 78
Asp	GAU	149.00	21 63	0.33
Asp	GAC	298 00	43 26	0 67
Val Val Val	GUG GUA GUU GUC	93 00 146 00 289 00 38 00	13 50 21 20 41 96 5 52	0 16 0 26 0 51 0 07
Ala	GCG	161 00	23.37	0 26
Ala	GCA	173 00	25 12	0 28
Ala	GCU	212 00	30 78	0 35
Ala	GCC	62 00	9 00	0 10
Arg	AGG	1.00	0 15	0 00
Arg	AGA	0.00	0 00	0 00
Ser	AGU	9.00	1 31	0 03
Ser	AGC	71.00	10 31	0 20
Lys	AAG	111 00	16 11	0 26
Lys	AAA	320 00	46 46	0 74
Asn	AAU	19.00	2 76	0 06
Asn	AAC	274 00	39 78	0 94
Met	AUG	170.00	24.68	1 00
Ile	AUA	1.00	0.15	0.00
Ile	AUU	70.00	10.16	0.17
Ile	AUC	345.00	50 09	0.83
Thr	ACG	25.00	3.63	0.07
Thr	ACA	14 00	2.03	0.04
Thr	ACU	130.00	18 87	0.35
Thr	ACC	206 00	29 91	0.55

Figure 9 (continued)

AmAcid	Codon	Number	/1000	Fraction
Trp	ugg	55 00	7 98	1 00
End	uga	0.00	0 00	0.00
Cys	ugu	22 00	3 19	0 49
Cys	ugc	23 00	3 34	0 51
End	UAG	0 00	0 00	0 00
End	UAA	0 00	0 00	0 00
Tyr	UAU	51.00	7 40	0 25
Tyr	UAC	157 00	22 79	0 75
Leu	UUG	18.00	2.61	0 03
Leu	UUA	12 00	1 74	0.02
Phe	UUU	51.00	7 40	0 24
Phe	UUC	166.00	24 10	0 76
Ser	UCG	14.00	2.03	0 04
Ser	UCA	7 00	1 02	0 02
Ser	UCU	120 00	17 42	0 34
Ser	UCC	131 00	19 02	0 37
Arg	CGG	1 00	0 15	0 00
Arg	CGA	2 00	0 29	0 01
Arg	CGU	290.00	42 10	0 74
Arg	CGC	96 00	13 94	0 25
Gln	CAG	233 00	33 83	0 86
Gln	CAA	37 00	5 37	0 14
His	CAU	18 00	2 61	0 17
His	CAC	85 00	12 34	0 83
Leu	CUG	480.00	69 69	0 83
Leu	CUA	2 00	0 29	0 00
Leu	CUU	25 00	3 63	0 04
Leu	CUC	38 00	5.52	0 07
Pro	CCG	190.00	27.58	0 77
Pro	CCA	36.00	5.23	0.15
Pro	CCU	19.00	2.76	0.08
Pro	CCC	1.00	0.15	0.00

Figure 10

Chromosomal localization of genes of the FGF family in $\operatorname{\mathsf{human}}$

Gene	Localization	Gene	Localization
FGF-1	5q31.3-q33.2	FGF-12	3g29-qter
FGF-2	4q26	FGF-13	X
FGF-3	11q13	FGF-14	13
FGF-4	11q13.3	(FGF-15)	
FGF-5	4g21	FGF-16	_
FGF-6	12p13	FGF-17	8p21
FGF-7	15q13-q22	FGF-18	5
FGF-8	10g25-g26	FGF-19	11q13.1
FGF-9	13q11-q12	FGF-20	8p21.3-p22
FGF-10	5p12-p13	FGF-21	19q13.1-qter
FGF-11	17	FGF-22	19p13.3
		FGF-23 □	12p13

Human FGF-15 gene has not been identified. The localization of human FGF-16 gene has not been determined.

Figure 11

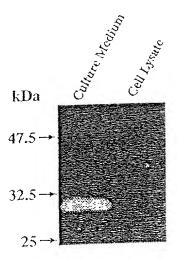


Figure 12

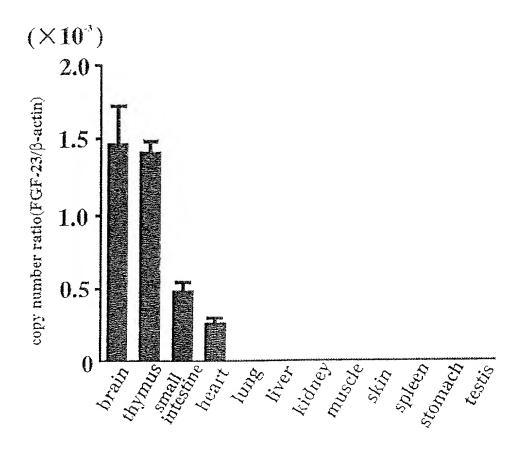


Figure 13

.

~28 kDa (6xHis-tagged)

~20 kDa (not tagged) + ~7-12 kDa (6xHis-tagged)

6XHis Tag

COMPACE ENTRY

	323	EGCRPFAKFI		: 5 5 7 t 2 9 1 :	! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! !		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	; } } !	;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		; ; ; ; ; ;	! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! !		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
	310	NTHAGGTGPE		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1111111111			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	: 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
	008	PLGWRGGR	1	1	WQDSTT	AS YEND ST	NKSKTT	NKSKTT		1 1 1 1 1	1	PS FEK	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	5	LGSQLEFSAH		ZRIKEREG-+		1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			1	
	290	SAEDNSPMASE			GTPTMNGGKVN	VSGVINGGKS	ASAIMNGGK PA	ASAIMNGGKP	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	PQPLT	PA	LVTGLEAVRS	1 1 1 1 1 1 1 1 1	PSQGRSPSYA	LEPSHVQASR	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	APPERUTUSVE	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ZEPP	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			
2	270 KUA 280	APASCSQELPS		PSSP	XGR-SRKSS	GSGTPTKSRS	GV-TPSKSTS	GV-TPSKSTS	1 1 1 1 1	TKRIBR	RIRPTH	PLETDSMOPFG		/GSSDPLSM/G	rrrokos pdn	1 1 1 1 1 1 1 1	PSPIKPKIPLS	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RSIRGSQRTWF	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	: : : : : : : : : : : : : : : : : : : :	1 1 1 1 1 1 1 1 1 1	
Č	00 020 020	NIKPRARMIP		Seganshisds	EPSIHEIGEKQGR-SRKSSGTPTMNGGKVVNQDST	EPSINDLIEFS-RSGSGTPTKSRSVSGVINGGKSMSHNEST-	·EPSIHDVGETVPKPGV-TPSKSTSASAIMNGGNPVNKSKTT	-EPSIHDVGETVPKPGV-TPSKSTSASAIMNGCKPVNKSKTT	RDLFHYR	KRL YOGOL PEPNHAEK-QKOFEFVGSAPTRATKRTRRPQPLT	OKPIKYTIVIKRSRRIRPTHPA	ANGELPISHFIRM PAYPEEPE-DIRGHIESDMFSSPIETDSMDPFGLVTGIEAVRSPSFEK		d-99094LID	PRPPGKGVQPI	1 1 1 1 1 1 1 1 1 1 1	LSFTVTVPEKIGPPSPIKPKIPLSAPRKUTNSVKYRLKFRFG	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		REFINYPPET	ELYKDILSQS	ELYKDLIMYT	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!	
7520 KDa	260	SAEDDSERDPL		1	1	1	1	1	PSMS	FPNHAEK-QKQ	LQKP	PE-DIR		P	EMVRQLQ-SGI	1	į.	1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TEQ-SLF	PEL	1	: : : : : : : : : : : : : : : : : : : :	
	0 250	NTPI PRRHTRS	LPLPWSSD	LPKILEVANYO	VPKPIEVCMYR	LPKPLKVAMYI	LPKPLEVAMYE	LPKPLEVAMY	LPREVDPSKL	TEMPLY OGOLP!	MARY PKGOPE	T.PMIL.PMVPEE	TEMSAKS	TRIPGLPPAL	T.PRMIDHROH	T.PR.L	TPREKOSEOP	T.PRIT	T.EMAIR	MEN PRCHHT	TLPREVDPDKV	T.PREWDPERVP		FLPR V
F 9713	230 KDa ₂₄₀	KCF2 (141) AKRAFIDGANPEPYSOFISRENEI PLIHENTPI PRRHTRSAEDDSERDPINVIKPRARMTPAPASCSQEI PSAEDNSPMASDPIGVVRGGRVNTHAGGIGPEGCRPFAKFI	MAN (17) MAFVGLANGSCRAGERIHYGORALLETE PAR (17) CHAIN NORGHBEBCOKEBBROHSEEFF	POST (170) PAYLIGLOROSOVAKOV — PAVROVIKADAH FLPKILISAVAYO — — —	PCF-12(172) PWFIGINAGIOIMKGN - PRWKATIKPSSHFVI	FGF13(168) GWYLGINKGPGEINKGNHVKRANKPARHFI.PKPLKVRMYK	PGF14(170) PWFIGINIGO AMKGN - PWROTIKPARHEL PKPLEVAMYR-	NFG-15(175) PWELGLANGORMKGNPWKKTKPAAHELPKPIAPLEVAMYR	RTKAHOKETHELPRAMPESKIPSMSRDLFHYR	RSRONOREAHFI	NPGF-18 (149) -WYVGFTERKGP-FKGP-FKTRENQODVH FNARK PKGQPEL	KARGFLPLEHE	KHGPGOKAIL) - LHUBURGNKS阿服RDEAPRGE-MRFINUPGLEPALEEPGILAPOPP-DVGSSDPLSYVGFSQGRSFSYAS	<u>w</u> yvsyngigarrork <u>trr</u> roks <u>sli</u> filprahemyrolo-sglprppgkgvopprrrokospdniepshvoasrigsolefsah	PLACE TO - METALOGO DE CONTRACTOR DE LA	RVKPOHISTHI	Prialskykagskvspimivihfipal	NOTE (162) EMEVALNOKGI PVRGK - KTKREOKTAH FLEMA(III	VYMAETIRIKARIPRKGSKTROHOREVHENGALPRGHHTTEQ-SLRFEFINYPPFTRSLRGSORIWAPEPP	PGP9(161) RYYVALINGGATPHESPRIKRHOKFIHFILPREPDRVP-	NPGP20(164) RY EVALNIKIZATPRICIARSKRHOK FITH FIL	hFGF-22Noou(139) —MET ALDRINGGERINGS——RTRRYHLSAHET.	RIKK AHFL.
11774		MNPBPYSOFL	NGSOKAGP	EGOVAKON	HOOTMAGN-	BARINKSN	HODAMAGN	ECONTRON-		NFGF-17 (149) - WEMAFTROGREPROGS	ACORPREGE-	LEVSISSAKO-HOLY	PRODUKTUS	NKSEEDDP	SKARPRRGF	CHANGE	会分文公司 SF	AYGRAKAGS	OKGIEVRGK	AKGRPRKGS	And PRESE	KOGIPHOGA	RRGGPR PGG	WYVAL K G PRKG
4-	(213) 213 KD 20	1) AKRAETTPG	1) NWEVGLESS	STATISTAME (O)	12) AWELGILY	38) GWYLGLNK	70) 学员员成	75) 岩町四日	SO dyrvailt	STEEPENEM (6)	49) JWYVGFT	41) - LRVSISS	3. 点YVALA	1	52) ILMYVSVNO	//)-MFIAID	87) EMYVAIN	79) - Trinis	62) EMEVALNO	67) -WYNAFT	61) RYYNHU	STRAILS (S)	39) -METAID	113) WYVAL
	(2)	FGF2 (1-	71) (1) (1) (1) (1) (1) (1) (1) (1) (1) (hAGF-11 (17	NAT-12(17	hPGP-13 (16	15年14(三	NATH-15(!)	11.01.16(1C	50年12年	1)81-4544	hPGF-19 (141)	hFGF-2 (123)	hFGF21 (143)	hPGF-3 (152) 11	こすられ	HPGP-5 PLIR 122 (187) EMYVALLAGAKAKARGOSBRANGPOHISTHAFLPRATKOSEOPE	NFGF-6 (179)	hFGF7(;	hFGF8(167) _	L) GEBON	1,007-041	L) MONTO HOLD	Consensus (213)

Fig. 15

Figure 16

